



SEQUENCE LISTING

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<120> ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR

<130> SCRIP1160-4

<140> US 09/500,700

<141> 2000-02-09

<150> US 08/863,813

<151> 1997-05-27

<150> US 08/676,318

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C4 <150> PCT/US95/00829

<151> 1995-01-18

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<160> 71

<170> PatentIn version 3.0

<210> 1

<211> 32

<212> PRT

<213> Xenopus

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<221> VARIANT

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<223> Xaa is any Amino Acid

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<222> (4)..(7)

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<222> (9)..(11)

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C4
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 <223> Xaa may be missing

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 <223> Xaa may be missing

<220>
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 <223> Xaa may be missing

<400> 1

Xaa Xaa Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Leu Xaa Xaa His Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

<210> 2
 <211> 36
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer for amplification of pZif89

<400> 2
 atgaaactgc tcgagcccta tgcttgccct gtcgag 36

<210> 3
 <211> 45
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer for amplification of pZif89

<400> 3
 gaggaggagg agactagtgt ccttctgtct taaatggatt ttggt 45

<210> 4
 <211> 273
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (1)..(273)

<400> 4
 ctc gag ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc ttt tct 48
 Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
 1 5 10 15

cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc cag aag 96
 Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys
 20 25 30

ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt gac cac 144
 Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His
 35 40 45

ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt gcc tgt 192

C4

Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
 50 55 60

gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag agg cat 240
 Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His
 65 70 75 80

acc aaa atc cat tta aga cag aag gac act agt 273
 Thr Lys Ile His Leu Arg Gln Lys Asp Thr Ser
 85 90

<210> 5
 <211> 91
 <212> PRT
 <213> Mouse

<400> 5

Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
 1 5 10 15

Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys
 20 25 30

Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His
 35 40 45

Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys
 50 55 60

Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His
 65 70 75 80

Thr Lys Ile His Leu Arg Gln Lys Asp Thr Ser
 85 90

<210> 6
 <211> 22
 <212> DNA
 <213> Artificial sequence

<220>
 <223> FTX3 primer

<400> 6
 gcaattaacc ctcactaaag gg 22

<210> 7
 <211> 21
 <212> DNA
 <213> Artificial sequence

<220>

<223> BZF3 primer

<400> 7

ggcaaacttc ctcccacaaa t

21

<210> 8

<211> 60

<212> DNA

<213> Artificial sequence

<220>

<223> ZF36K primer

<220>

<221> misc_feature

<222> (22)..(41)

<223> n is any nucleotide

<400> 8

atttgtggga ggaagtttgc cnnkagtnnk nnknnknnkn nkcataccaa aatccattta

60

<210> 9

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> R3B primer

<400> 9

ttgatattca caaacgaatg g

21

<210> 10

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> ZFNsiB primer

<400> 10

catgcatatt cgacactgga a

21

<210> 11

<211> 66

<212> DNA

<213> Artificial sequence

<220>

<223> ZF2r6F primer

<220>

<221> misc_feature

<222> (28)..(44)

<223> n is any nucleotide

c4

<400> 11
 cagtgtcgaa tatgcatgcg taacttcnnk nnknnknnkn nknnkaccac ccacatccgc 60
 acccac 66

<210> 12
 <211> 66
 <212> DNA
 <213> Artificial sequence

<220>
 <223> ZFI6rb primer

<220>
 <221> misc_feature
 <222> (26)..(45)
 <223> n is any nucleotide

c4
 <400> 12
 ctggcctgtg tggatgcgga tatgmnnmnn mnnmnnmnnnc gamnnagaaa agcggcgatc 60
 gcagga 66

<210> 13
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> ZFIF primer

<400> 13
 catatccgca tccacacagg ccag 24

<210> 14
 <211> 8
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Modified sequence of finger 1 of zif268

<400> 14

Arg Ser Asp Glu Leu Thr Arg His
 1 5

<210> 15
 <211> 6
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Modified sequence of finger 2 of zif268

<400> 15

Ser Arg Ser Asp His Leu
1 5

<210> 16
<211> 34
<212> DNA
<213> Artificial sequence

<220>
<223> Hairpin oligonucleotide of a phage library containig phages

<400> 16
cgtaaattggg cgcccttttg ggcgcccatt tacg

34

<210> 17
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Binding sequence of zif268 finger 3

<400> 17

Arg Ser Asp Glu Arg Lys Arg His
1 5

<210> 18
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Binding sequence of zif268 finger 3

<400> 18

Trp Ser Ile Pro Val Leu Leu His
1 5

<210> 19
<211> 8
<212> PRT
<213> Artificial sequence

<220>
<223> Binding sequence of zif268 finger 3

<400> 19

Trp Ser Leu Leu Pro Val Leu His
1 5

<210> 20
<211> 8
<212> PRT
<213> Artificial sequence

<220>

<223> Binding sequence of zif268 finger 3

<400> 20

Phe Ser Phe Leu Leu Pro Leu His
1 5

<210> 21

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Binding sequence of zif268 finger 3

<400> 21

Leu Ser Thr Trp Arg Gly Trp His
1 5

<210> 22

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Binding sequence of zif268 finger 3

<400> 22

Thr Ser Ile Gln Leu Pro Tyr His
1 5

<210> 23

<211> 61

<212> DNA

<213> Homo sapiens

<400> 23

tgatctcaga agccaagcag ggtcgggcct ggtagtact tggatgggag accgcctggg 60

a 61

<210> 24

<211> 26

<212> PRT

<213> Homo sapiens

<400> 24

Tyr Ile Cys Ser Phe Ala Asp Cys Gly Ala Ala Tyr Asn Lys Asn Trp
1 5 10 15

Lys Leu Gln Ala His Leu Cys Lys His Thr
20 25

<210> 25

<211> 26

<212> PRT

<213> Homo sapiens

<400> 25

Phe Pro Cys Lys Glu Glu Gly Cys Glu Lys Gly Phe Thr Ser Leu His
1 5 10 15

His Leu Thr Arg His Ser Leu Thr His Thr
20 25

<210> 26

<211> 26

<212> PRT

<213> Homo sapiens

<400> 26

Phe Thr Cys Asp Ser Asp Gly Cys Asp Leu Arg Phe Thr Thr Lys Ala
1 5 10 15

Asn Met Lys Lys His Phe Asn Arg Phe His
20 25

<210> 27

<211> 13

<212> DNA

<213> Homo sapiens

<400> 27

tggatgggag acc

13

<210> 28

<211> 8

<212> PRT

<213> Artificial sequence

<220>

<223> Binding sequence of zif268 finger 3

<400> 28

Arg Ser Asp Glu Arg Lys Arg His
1 5

<210> 29

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Primer for amplification of fragments of zif268

<400> 29

gtccataaga ttagcggatc c

21

<210> 30

<211> 21

<212> DNA

<213> Artificial sequence

<220>
 <223> Primer for amplification of fragments of zif268

 <400> 30
 gtgagcgagg aagcggaaga g 21

 <210> 31
 <211> 34
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> zif268 consensus binding site

 <400> 31
 cctgctgagg cgcccttttg ggcgcccacg cagg 34

 <210> 32
 <211> 4
 <212> PRT
 <213> Artificial sequence

 <220>
 <223> Linker peptide

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 <221> VARIANT
 <222> (4)..(4)
 <223> Xaa is Lys or Pro

 <400> 32

 Thr Gly Glu Xaa
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 <210> 33
 <211> 462
 <212> DNA
 <213> Mouse

 <220>
 <221> CDS
 <222> (1)..(459)

 <400> 33
 atg ctc gag ctc ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc 48
 Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
 1 5 10 15

 ttt tct cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc 96
 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
 20 25 30

 cag aag ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt 144
 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
 35 40 45

 gac cac ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt 192

Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
 50 55 60
 gcc tgt gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag 240
 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
 65 70 75 80
 agg cat acc aaa atc cat acc ggr cag aag ccc act agt ggc ggt ggt 288
 Arg His Thr Lys Ile His Thr Xaa Gln Lys Pro Thr Ser Gly Gly Gly
 85 90 95
 cgg atc gcc cgg ctg gag gaa aaa gtg aaa acc ttg aaa gcg caa aac 336
 Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn
 100 105 110
 tcc gag ctg gcg tcc acc cgg aac atg ctc agg gaa cag gtg gca cag 384
 Ser Glu Leu Ala Ser Thr Arg Asn Met Leu Arg Glu Gln Val Ala Gln
 115 120 125
 ctt aaa cag aaa gtc atg aac cac gct agc ggc cag gcc ggc cag tac 432
 Leu Lys Gln Lys Val Met Asn His Ala Ser Gly Gln Ala Gly Gln Tyr
 130 135 140
 ccg tac gac gtt ccg gac tac gct tct taa 462
 Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 145 150

<210> 34
 <211> 153
 <212> PRT
 <213> Mouse

<400> 34

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
 1 5 10 15
 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
 20 25 30
 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
 35 40 45
 Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
 50 55 60
 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
 65 70 75 80
 Arg His Thr Lys Ile His Thr Xaa Gln Lys Pro Thr Ser Gly Gly Gly
 85 90 95
 Arg Ile Ala Arg Leu Glu Glu Lys Val Lys Thr Leu Lys Ala Gln Asn
 100 105 110

Ser Glu Leu Ala Ser Thr Arg Asn Met Leu Arg Glu Gln Val Ala Gln
 115 120 125

Leu Lys Gln Lys Val Met Asn His Ala Ser Gly Gln Ala Gly Gln Tyr
 130 135 140

Pro Tyr Asp Val Pro Asp Tyr Ala Ser
 145 150

<210> 35
 <211> 462
 <212> DNA
 <213> Mouse

<220>
 <221> CDS
 <222> (1)..(459)

<400> 35
 atg ctc gag ctc ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc 48
 Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
 1 5 10 15

ttt tct cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc 96
 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
 20 25 30

cag aag ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt 144
 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
 35 40 45

gac cac ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt 192
 Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
 50 55 60

gcc tgt gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag 240
 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
 65 70 75 80

agg cat acc aaa atc cat acc ggt cag aag ccc act agt ggc ggt ggt 288
 Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly
 85 90 95

ctg acc gac acc ctg cag gcg gaa acc gac cag ctg gaa gac gaa aaa 336
 Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys
 100 105 110

tcc gcg ctg caa acc gaa atc gcg aac ctg ctg aaa gaa aaa gaa aag 384
 Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys
 115 120 125

ctg gag ttc atc ctg gcg gca cac gct agc ggc cag gcc ggc cag tac 432
 Leu Glu Phe Ile Leu Ala Ala His Ala Ser Gly Gln Ala Gly Gln Tyr
 130 135 140

ccg tac gac gtt ccg gac tac gct tct taa 462

Pro Tyr Asp Val Pro Asp Tyr Ala Ser
145 150

<210> 36
<211> 153
<212> PRT
<213> Mouse

<400> 36

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
1 5 10 15

Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
20 25 30

Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
35 40 45

Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
50 55 60

Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
65 70 75 80

Arg His Thr Lys Ile His Thr Gly Gln Lys Pro Thr Ser Gly Gly Gly
85 90 95

Leu Thr Asp Thr Leu Gln Ala Glu Thr Asp Gln Leu Glu Asp Glu Lys
100 105 110

Ser Ala Leu Gln Thr Glu Ile Ala Asn Leu Leu Lys Glu Lys Glu Lys
115 120 125

Leu Glu Phe Ile Leu Ala Ala His Ala Ser Gly Gln Ala Gly Gln Tyr
130 135 140

Pro Tyr Asp Val Pro Asp Tyr Ala Ser
145 150

<210> 37
<211> 19
<212> DNA
<213> Artificial sequence

<220>

<223> Single stranded leucine zipper domain of zif268-Jun

<220>

<221> misc_feature

<222> (10)..(10)
 <223> n is any nucleotide. n can be any number of nucleotides

<400> 37
 cgcccacgcn gcgtgggcg

19

<210> 38
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Single-stranded leucine zipper domain of zif268-Fos

<220>
 <221> misc_feature
 <222> (10)..(10)
 <223> n is any nucleotide. n can be any number of nucleotides

<400> 38
 cgcccacgcn gcggcggcgg cggcggcg

28

<210> 39
 <211> 76
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Construction of C7 zinc finger

<220>
 <221> VARIANT
 <222> (76)..(76)
 <223> Xaa is Tyr-Ala-Cys-Pro-Val-Glu-Ser-Cys-Asp-Arg-Arg-Phe-Ser-Lys-Se
 r-Ala-Asp-Leu-Lys-His-Ile-Arg-His-Thr-Gly-Glu-Lys-Pro-Met-Lys-Leu
 -Leu-Glu-Pro-repeated 10 times; residue 76=340 Amino Acids; some
 Xaa's may be missing

<400> 39

Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg
 1 5 10 15

Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg His Thr Gly
 20 25 30

Glu Lys Pro Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser
 35 40 45

Cys Asp Arg Arg Phe Ser Lys Ser Ala Asp Leu Lys His Ile Arg His
 50 55 60

Thr Gly Glu Lys Pro Met Lys Leu Leu Glu Pro Xaa
 65 70 75

<210> 40

<211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Oligonucleotide hairpin

<400> 40
 cctcgccgcc gcgggttttc ccgcgcccc gagg 34

<210> 41
 <211> 294
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(294)

<400> 41
 atg aaa ctg ctc gag ccc tat gct tgc cct gtc gag tcc tgc gat cgc 48
 Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg
 1 5 10 15
 cgc ttt tct aag tcg gct gat ctg aag cgc cat atc cgc atc cac act 96
 Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr
 20 25 30
 ggc gaa aaa ccg tac gcg tgc cct gtc gag tcc tgc gat cgc cgc ttt 144
 Gly Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe
 35 40 45
 tct aag tcg gct gat ctg aag cgc cat atc cgc atc cac acc ggg gag 192
 Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Glu
 50 55 60
 aag ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc ttt tct aag 240
 Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Lys
 65 70 75 80
 tcg gct gat ctg aag cgc cat atc cgc atc cac acc ggt cag aag ccc 288
 Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
 85 90 95
 act act 294
 Thr Thr

<210> 42
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 42
 Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg
 1 5 10 15

Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr
 20 25 30

Gly Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe
 35 40 45

Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Glu
 50 55 60

Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Lys
 65 70 75 80

Ser Ala Asp Leu Lys Arg His Ile Arg Ile His Thr Gly Gln Lys Pro
 85 90 95

Thr Thr

<210> 43
 <211> 543
 <212> DNA
 <213> Artificial sequence

<220>
 <223> zif268-zif268 with TGEKP linker

<220>
 <221> CDS
 <222> (1)..(543)

<400> 43
 atg ctc gag ctc ccc tat gct tgc cct gtc gag tcc tgc gat cgc cgc 48
 Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
 1 5 10 15
 ttt tct cgc tcg gat gag ctt acc cgc cat atc cgc atc cac aca ggc 96
 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
 20 25 30
 cag aag ccc ttc cag tgt cga ata tgc atg cgt aac ttc agt cgt agt 144
 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
 35 40 45
 gac cac ctt acc acc cac atc cgc acc cac aca ggc gag aag cct ttt 192
 Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
 50 55 60
 gcc tgt gac att tgt ggg agg aag ttt gcc agg agt gat gaa cgc aag 240
 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
 65 70 75 80
 agg cat acc aaa atc cat acc ggg gag aag ccc tat gct tgc cct gtc 288
 Arg His Thr Lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val
 85 90 95

gag tcc tgc gat cgc cgc ttt tct cgc tcg gat gag ctt acc cgc cat 336
 Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His
 100 105 110
 atc cgc atc cac aca ggc cag aag ccc ttc cag tgt cga ata tcc atg 384
 Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Ser Met
 115 120 125
 cgt aac ttc agt cgt agt gac cac ctt acc acc cac atc cgc acc cac 432
 Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His
 130 135 140
 aca ggc gag aag cct ttt gcc tgt gac att tgt ggg agg aag ttt gcc 480
 Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
 145 150 155 160
 agg agt gat gaa cgc aag agg cat acc aaa atc cat tta aga cag aag 528
 Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys
 165 170 175
 gac tct aga act agt 543
 Asp Ser Arg Thr Ser
 180

<210> 44
 <211> 181
 <212> PRT
 <213> Artificial sequence

<220>
 <223> zif268-zif268 with TGEKP linker

<400> 44

Met Leu Glu Leu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg
 1 5 10 15
 Phe Ser Arg Ser Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly
 20 25 30
 Gln Lys Pro Phe Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser
 35 40 45
 Asp His Leu Thr Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe
 50 55 60
 Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys
 65 70 75 80
 Arg His Thr Lys Ile His Thr Gly Glu Lys Pro Tyr Ala Cys Pro Val
 85 90 95
 Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His
 100 105 110

Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Ser Met
 115 120 125

Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His
 130 135 140

Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
 145 150 155 160

Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys
 165 170 175

Asp Ser Arg Thr Ser
 180

<210> 45
 <211> 46
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer for generation of 5' C7

<400> 45
 gaggaggagg agggatccat gctcgagctc ccctatgctt gccctg 46

<210> 46
 <211> 39
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer for generation of 5' C7

<400> 46
 gaggaggaga ccggtatgga ttttggtatg cctcttgcg 39

<210> 47
 <211> 57
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer for generation of 3' C7

<400> 47
 gaggaggaga ccggtgagaa gccctatgct tgccctgtcg agtcctgcga tcgccgc 57

<210> 48
 <211> 32
 <212> DNA

<213> Artificial sequence

<220>

<223> Primer for generation of 3' C7

<400> 48

gaggaggaga ctagttctag agtccttctg tc

32

<210> 49

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Primary strand within a duplex region of a probe for C7-C7 site

<400> 49

gatgtatgta gcgtgggcgg cgtgggcgta agtaatgc

38

<210> 50

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Primary strand within a duplex region of a probe for SP1C-C7 site

<400> 50

gatgtatgta gcgtgggcgg gggcggggta agtaatgc

38

<210> 51

<211> 38

<212> DNA

<213> Artificial sequence

<220>

<223> Primary strand within a duplex region of a probe for (GCG)6 site

<400> 51

gatgtatgta gcggcggcgg cggcggcgta agtaatgc

38

<210> 52

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Primary strand within a duplex region of a probe for C7 site

<400> 52

gatgtatgta gcgtgggcgt aagtaatgc

29

<210> 53

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Primary strand within a duplex region of a probe for Sp1C site

<400> 53

gatgtatgta ggggcggggt aagtaatgc

29

<210> 54

<211> 29

<212> DNA

<213> Artificial sequence

<220>

<223> Primer

<400> 54

gatgtatgta gcgtgggcgt aagtaatgc

29

<210> 55

<211> 41

<212> DNA

<213> Artificial sequence

<220>

<223> EcoRIfootF primer

<400> 55

gaggaggagg aattccgaca ttataatga acgtgaattg c

41

<210> 56

<211> 45

<212> DNA

<213> Artificial sequence

<220>

<223> C7-C73>5 primer

<400> 56

tgcgccacg ccgccacgc gatgattggg agcttttttt gcacg

45

<210> 57

<211> 51

<212> DNA

<213> Artificial sequence

<220>

<223> C7-C75>3 primer

<400> 57

tcgcgtgggc ggcgtgggcg caaaaaatta ttatcatgga ttctaaaacg g

51

<210> 58

<211> 42

<212> DNA

<213> Artificial sequence

<220>
 <223> NotIfootB primer

<400> 58
 gaggaggagg cggccgcagg tagatgagat gtgacgaacg tg 42

<210> 59
 <211> 45
 <212> DNA
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 <223> Sp1C-C73>5 primer

<400> 59
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<210> 60
 <211> 51
 <212> DNA
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<220>
 <223> Sp1C75>3 primer

<400> 60
 tcgctgtgggc gggggcgggg caaaaaatta ttatcatgga ttctaaaacg g 51

<210> 61
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Target sequence of six finger protein C7-C7

<400> 61
 gcgtgggacg cgtgggacg 18

<210> 62
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Target sequence of six-finger protein Sp1C-C7

<400> 62
 gcgtgggacg gggcgggg 18

<210> 63
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Altered zif268 finger 1 binding site

<400> 63
 cctgcgtggt gtcccttttg ggacacaacg cagg

34

<210> 64
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Altered zif268 finger 2 binding site

<400> 64
 cctgcgttgg cgcccttttg ggcgccaacg cagg

34

<210> 65
 <211> 34
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Altered zif268 finger 3 binding site

<400> 65
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34

<210> 66
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker peptide

<400> 66

Thr Gly Gln Lys Pro
 1 5

<210> 67
 <211> 5
 <212> PRT
 <213> Artificial sequence

<220>
 <223> Linker peptide

<400> 67

Thr Gly Glu Lys Pro
 1 5

<210> 68
 <211> 18
 <212> DNA
 <213> Artificial sequence

<220>
<223> Sp1C-C7 probe

<400> 68
gcgtgggagg gggcgggg

18

<210> 69
<211> 18
<212> DNA
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<220>
<223> (GCG)6 probe

<400> 69
gcggcggcgg cggcggcg

18

<210> 70
<211> 6
<212> PRT
<213> Artificial sequence

<220>
<223> SV40 large T antigen

<400> 70

Pro Lys Lys Arg Lys Val
1 5

<210> 71
<211> 64
<212> PRT
<213> Artificial sequence

<220>
<223> Construction of C7 zinc finger

<400> 71

Met Lys Leu Leu Glu Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg
1 5 10 15

Arg Phe Ser Lys Ser Ala Asp Leu Lys Arg His Ile Arg His Thr Gly
20 25 30

Glu Lys Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser
35 40 45

Lys Ser Ala Asp Leu Lys His Ile Arg Ile His Thr Gly Glu Lys Pro
50 55 60

*C4
conc*